	Туре	Hits	Search Text	DBs
1	BRS	3	"200026358"	USPAT; US-PGPUB; EPO; JPO; DERWENT;
2	BRS	602	toji	USPAT; US-PGPUB; EPO; JPO; DERWENT;
3	BRS	7	toji and yano	USPAT; US-PGPUB; EPO; JPO; DERWENT;
4	BRS	2	JP05984	USPAT; US-PGPUB; EPO; JPO; DERWENT;
5	BRS	2	"20030167524"	USPAT; US-PGPUB; EPO; JPO; DERWENT;
6	BRS	1	"200151638"	USPAT; US-PGPUB; EPO; JPO; DERWENT;

```
RESULT 1
S66677
thioredoxin-disulfide reductase (EC 1.8.1.9) [validated] - human
N; Contains: thioredoxin reductase (NADPH), placental form; thioredoxin reductase
(NADPH), T-cell form
C; Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 10-Oct-1997 #text_change 03-Jun-2002
C; Accession: S66677; S74270; A43122; G01120
R; Gasdaska, P.Y.; Gasdaska, J.R.; Cochran, S.; Powis, G.
FEBS Lett. 373, 5-9, 1995
A; Title: Cloning and sequencing of a human thioredoxin reductase.
A; Reference number: S66677; MUID: 96013875; PMID: 7589432
A; Accession: S66677
A; Molecule type: mRNA
A; Residues: 1-497 < GAS1>
A; Cross-references: EMBL: X91247; NID: g1237037; PIDN: CAA62629.1; PID: g1237038;
GB:S79851; NID:g1184536; PID:g1184537
A; Accession: S74270
A; Molecule type: protein
A; Residues: 3-11;157-165;435-457 < GAS2 >
R; Gladyshev, V.N.; Jeang, K.T.; Stadtman, T.C.
Proc. Natl. Acad. Sci. U.S.A. 93, 6146-6151, 1996
A; Title: Selenocysteine, identified as the penultimate C-terminal residue in
human T-cell thioredoxin reductase, corresponds to TGA in the human placental
A; Reference number: A43122; MUID: 96234105; PMID: 8650234
A; Accession: A43122
A; Molecule type: protein
A; Residues: 488-497, 'X', 499 < GLA>
A; Note: the residue designated 'X' was determined to be selenocysteine; we have
shown the residue as Cys
C; Comment: In most tissues, such as placenta, the UGA codon is used as the
terminator. In the T-cell at least the UGA codon is translated with
selenocysteine, and termination occurs at a UAA codon two codons further along.
C; Genetics:
A; Gene: GDB: TXNRD1; TXNR
A; Cross-references: GDB:683567; OMIM:601112
A; Map position: 12q23-12q24.1
C; Complex: homodimer
C; Function:
A; Description: catalyzes the reduction of thioredoxin by NADPH
A; Note: the T-cell form also has peroxidase activity
C; Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase
homology
C; Keywords: alternative termination; FAD; flavoprotein; homodimer; NADP;
oxidoreductase; redox-active disulfide; selenocysteine
F;3-499/Product: thioredoxin reductase (NADPH), T-cell form #status experimental
<MAT1>
F;3-497/Product: thioredoxin reductase (NADPH), placental form #status
experimental <MAT2>
F;14-42/Region: beta-alpha-beta FAD nucleotide-binding fold
F;16-479/Domain: dihydrolipoamide dehydrogenase homology <DLD>
F;192-222/Region: beta-alpha-beta NADP nucleotide-binding fold
F;59-64/Disulfide bonds: redox-active #status predicted
F;472/Active site: His #status predicted
F;498/Modified site: selenocysteine #status experimental
```

Query Ma		52.1%; Score 1429; DB 1; Length 499; Similarity 56.0%; Pred. No. 6.8e-97;	
		4; Conservative 77; Mismatches 134; Indels 4; Gaps	2;
Qy	36	DYDLLVVGGGSGGLACAKEAAQLGRKVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMH	95
Db	12	DYDLIIIGGGSGGLAAAKEAAQYGKKVMVLDFVTPTPLGTRWGLGGTCVNVGCIPKKLMH	71
Qy	96	QAALLGGLIQDAPNYGWEVAQPVPHDWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIK	155
Db	72	QAALLGQALQDSRNYGWKVEETVKHDWDRMIEAVQNHIGSLNWGYRVALREKKVVYENAY	131
Qy	156	ASFVDEHTVCGVAKGGKEILLSADHIIIATGGRPRYPTHIEGALEYGITSDDIFWLKESP  :  :    :    :	215
Db	132	GQFIGPHRIKATNNKGKEKIYSAESFLIATGERPRY-LGIPGDKEYCISSDDLFSLPYCP	190
Qу	216	GKTLVVGASYVALECAGFLTGIGLDTTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRG	275
Db	191	GKTLVVGASYVALECAGFLAGIGLGVTVMVRSILLRGFDQDMANKIGEHMEEHGIKFIRQ	250
Qy	276	CAPSRVRRLPDGQLQVTWEDSTTGKEDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTS   :   ::   ::   ::   ::   ::   ::   ::	332
Db	251	FVPIKVEQIEAGTPGRLRVVAQSTNSEEIIEGEYNTVMLAIGRDACTRKIGLETVGVKIN	310
Qy	333	PDTQKILVDSREATSVPHIYAIGDVVEGRPELTPTAIMAGRLLVQRLFGGSSDLMDYDNV	392
Db	311	EKTGKIPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGRLLAQRLYAGSTVKCDYENV	370
Qy	393	PTTVFTPLEYGCVGLSEEEAVARHGQEHVEVYHAHYKPLEFTVAGRDASQCYVKMVCLRE	452
Db	371	PTTVFTPLEYGACGLSEEKAVEKFGEENIEVYHSYFWPLEWTIPSRDNNKCYAKIICNTK	430
Qy	453	PPQLVLGLHFLGPNAGEVTQGFALGIKCGASYAQVMRTVGIHPTCSEEVVKLRISKRSGL:  :	512
Db	431	DNERVVGFHVLGPNAGEVTQGFAAALKCGLTKKQLDSTIGIHPVCAEVFTTLSVTKRSGA	490
Qy	513	DPTVTGCXG 521	
Db	491	SILQAGCCG 499	

•

```
RESULT 1
US-10-032-201B-297
; Sequence 297, Application US/10032201B
 Publication No. US20030167524A1
; GENERAL INFORMATION:
  APPLICANT: Van Rooijen, Gijs
  APPLICANT: Deckers, Harm
  APPLICANT: Heifetz, Peter Bernard
  APPLICANT: Briggs, Steven
  APPLICANT: Dalmia, Bipin Kumar
  APPLICANT: Del Val, Greg
  APPLICANT: Zaplachinski, Steve
  APPLICANT: Moloney, Maurice
  TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND
RELATED
  TITLE OF INVENTION: COMPOSITIONS
  FILE REFERENCE: 38814 351B
  CURRENT APPLICATION NUMBER: US/10/032,201B
  CURRENT FILING DATE: 2001-12-19
  NUMBER OF SEQ ID NOS: 313
  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 297
   LENGTH: 494
   TYPE: PRT
   ORGANISM: Homo sapien
US-10-032-201B-297
 Query Match
                      93.7%; Score 488; DB 12; Length 494;
 Best Local Similarity
                      100.0%; Pred. No. 0;
 Matches 488; Conservative 0; Mismatches
                                          0; Indels
                                                      0; Gaps
                                                                0;
Qу
         32 AGQRDYDLLVVGGGSGGLACAKEAAQLGRKVAVVDYVEPSPQGTRWGLGGTCVNVGCIPK 91
            Db
          5 AGQRDYDLLVVGGGSGGLACAKEAAQLGRKVAVVDYVEPSPQGTRWGLGGTCVNVGCIPK 64
Qу
         92 KLMHQAALLGGLIQDAPNYGWEVAQPVPHDWRKMAEAVQNHVKSLNWGHRVQLQDRKVKY 151
            65 KLMHQAALLGGLIQDAPNYGWEVAQPVPHDWRKMAEAVQNHVKSLNWGHRVQLQDRKVKY 124
Db
Qу
        152 FNIKASFVDEHTVCGVAKGGKEILLSADHIIIATGGRPRYPTHIEGALEYGITSDDIFWL 211
            Db
        125 FNIKASFVDEHTVCGVAKGGKEILLSADHIIIATGGRPRYPTHIEGALEYGITSDDIFWL 184
Qy
        212 KESPGKTLVVGASYVALECAGFLTGIGLDTTIMMRSIPLRGFDQQMSSMVIEHMASHGTR 271
            Db
        185 KESPGKTLVVGASYVALECAGFLTGIGLDTTIMMRSIPLRGFDQQMSSMVIEHMASHGTR 244
Qу
        272 FLRGCAPSRVRRLPDGQLQVTWEDSTTGKEDTGTFDTVLWAIGRVPDTRSLNLEKAGVDT 331
            Db
        245 FLRGCAPSRVRRLPDGQLQVTWEDSTTGKEDTGTFDTVLWAIGRVPDTRSLNLEKAGVDT 304
Qу
        332 SPDTQKILVDSREATSVPHIYAIGDVVEGRPELTPTAIMAGRLLVQRLFGGSSDLMDYDN 391
            Db
        305 SPDTQKILVDSREATSVPHIYAIGDVVEGRPELTPTAIMAGRLLVQRLFGGSSDLMDYDN 364
Qу
        392 VPTTVFTPLEYGCVGLSEEEAVARHGOEHVEVYHAHYKPLEFTVAGRDASOCYVKMVCLR 451
```

Db		
Qу	452 EPPQLVLGLHFLGPNAGEVTQGFALGIKCGASYAQVMRTVGIHPTCSEEVVKLRIS	
Db	425 EPPQLVLGLHFLGPNAGEVTQGFALGIKCGASYAQVMRTVGIHPTCSEEVVKLRIS	
Qу	512 LDPTVTGC 519	
Db	485 LDPTVTGC 492	

•

```
RESULT 3
ABP60944
     ABP60944 standard; Protein; 521 AA.
XX
AC
     ABP60944;
XX
DT
     06-SEP-2002 (first entry)
XX
DE
     Homo sapiens thioredoxin reductase SEQ ID NO:293.
XX
KW
     Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KW
     oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
     vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;
KW
     food product; milk; wheat; oxidative stress; cataract; diabetes;
KW
KW
     chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW
     bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW
     gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW
     gastro oesophageal reflux disease.
XX
OS
     Homo sapiens.
XX
PN
     WO200250289-A1.
XX
PD
     27-JUN-2002.
XX
PF
     19-DEC-2001; 2001WO-US50240.
XX
     19-DEC-2000; 2000US-0742900.
PR
PR
     05-JUL-2001; 2001US-302885P.
PR
     04-DEC-2001; 2001US-0006038.
XX
PA
     (SEMB-) SEMBIOSYS GENETICS INC.
PΑ
     (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
     Van Rooijen G, Deckers H, Heifetz PB,
ΡI
                                              Briggs SP, Dalmia BK;
PΙ
     Del Val G, Zaplachinski S, Moloney M;
XX
DR
     WPI; 2002-508806/54.
XX
PT
     Producing oil body associated with recombinant multimeric protein
PT
     complex e.g. redox proteins and immunoglobulins comprises producing
PT
     recombinant polypeptides capable of forming the complex in cells
PT
     comprising oil bodies -
XX
PS
     Claim 82; Page 337-338; 362pp; English.
XX
CC
     The present invention describes a method (M1) for producing an oil body
CC
     associated with a recombinant multimeric protein complex (MPC). M1
CC
     comprises producing in a cell comprising oil bodies a first and second
CC
     recombinant polypeptide (P1, P2), where P1 is capable of associating
     with P2 to form the MPC and associating the complex with an occlusion
CC
CC
     body (OB) through an OB-targeting-protein capable of associating with OB
CC
     and P1. M1 is useful for producing an oil body associated with a
CC
     recombinant MPC. The oil bodies are further formulated for use in the
CC
    preparation of a food product such as milk or wheat based food product,
CC
    personal care product which reduces the oxidative stress on the surface
     area of the human body or used to lighten the skin, or a pharmaceutical
CC
```

```
CC
    composition used to treat chronic obstructive pulmonary disease (COPD),
CC
    cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC
    malignancies, reperfusion injury, wound healing, sepsis, qastro
CC
    intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC
    (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
CC
    to ABP60964 represent sequence given in the exemplification of the
CC
    present invention.
XX
SQ
    Sequence
            521 AA;
 Query Match
                    99.7%; Score 2736; DB 23; Length 521;
 Best Local Similarity 99.8%; Pred. No. 2.8e-253;
 Matches 520; Conservative
                          0; Mismatches
                                           Indels
                                                      Gaps
                                                             0;
Qу
         1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
           Db
         1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAOLGR 60
        61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Qу
           DЪ
        61 KVAVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHOAALLGGLIODAPNYGWEVAOPVPH 120
Qу
       121 DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
           Db
       121 DWRKMAEAVONHVKSLNWGHRVOLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
       181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
           181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Db
       241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
Qу
           Db
       241 TTIMMRSIPLRGFDQOMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
       301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTOKILVDSREATSVPHIYAIGDVVEG 360
Qу
           Db
       301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTOKILVDSREATSVPHIYAIGDVVEG 360
       361 RPELTPTAIMAGRLLVORLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGOEH 420
Qу
           361 RPELTPIAIMAGRLLVORLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGOEH 420
Db
Qу
       421 VEVYHAHYKPLEFTVAGRDASOCYVKMVCLREPPOLVLGLHFLGPNAGEVTOGFALGIKC 480
           Db
       421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTOGFALGIKC 480
       481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Qу
           481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Db
```

```
RESULT 6
AAE05190
ID
     AAE05190 standard; Protein; 522 AA.
XX
AC
     AAE05190;
XX
DT
     12-SEP-2001 (first entry)
XX
DE
     Human drug metabolising enzyme (DME-21) protein.
XX
KW
     Human; drug metabolising enzyme; DME-21; immunosuppressive; gene therapy;
KW
     cytostatic; autoimmune disorder; inflammatory disorder; atherosclerosis;
KW
     osteoporosis; eye disorder; hepatic tumour; Addison's disease; cretinism;
KW
     rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia;
KW
     developmental disorder; endocrine disorder; iritis; acromegaly; epilepsy;
KW
     thyrotoxicosis; pancreatic disorder; diabetes mellitus; obesity; adenoma;
KW
     gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma;
KW
     actinic keratosis; metabolic disorder; dysphagia; anorexia; carcinoma;
KW
     cell proliferative disorder.
XX
OS
     Homo sapiens.
XX
PN
     WO200151638-A2.
XX
PD
     19-JUL-2001.
XX
     12-JAN-2001; 2001WO-US01174.
PF
XX
PR
     14-JAN-2000; 2000US-0176139.
PR
     21-JAN-2000; 2000US-0177443.
PR
     28-JAN-2000; 2000US-0178574.
XX
PΑ
     (INCY-) INCYTE GENOMICS INC.
XX
ΡI
     Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM,
PΙ
     Ring HZ, Hillman JL, Yue H, Azimzai Y, Yao MG, Gandhi AR;
PΙ
     Nguyen DB, Tang YT, Lal P, Bandman O;
XX
DR
     WPI; 2001-425874/45.
DR
     N-PSDB; AAD09956.
XX
PT
     Drug metabolizing enzymes and encoding polynucleotides, useful for
     diagnosing, treating and/or preventing autoimmune, inflammatory, cell
PT
PT
     proliferative, developmental, endocrine, eye, metabolic, and
PΤ
     gastrointestinal disorders -
XX
PS
     Claim 1; Page 155-156; 133pp; English.
XX
CC
     The present sequence is human drug metabolising enzyme (DME-21) protein.
     Human DME and its nucleic acid molecule are useful for the diagnosis,
CC
CC
     treatment and prevention of disorders associated with increased or
CC
     decreased expression of DME. Examples of such disorders include,
     autoimmune/inflammatory disorder such as acquired immune deficiency
CC
CC
     syndrome (AIDS), rheumatoid arthritis, osteoporosis; cell proliferative
     disorder such as actinic keratosis, atherosclerosis; developmental
CC
CC
     disorder such as epilepsy, anaemia; endocrine disorder such as
CC
     acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as
```

```
diabetes mellitus; eye disorder such as conjunctivitis, glaucoma, iritis;
CC
    metabolic disorder such as Addison's disease, obesity; gastrointestinal
CC
    disorder such as anorexia, dysphagia and hepatic tumours including
CC
    nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for
CC
    creating `knockin' humanised animals (pigs) or transgenic animals (mice
CC
    or rats) to model human disease. DME DNA is also in useful is gene
CC
CC
    therapy. DME and its immunogenic fragments are useful for screening
    libraries of compounds in several drug screening assays.
CC
XX
SO
    Sequence
            522 AA;
                     99.5%; Score 2729; DB 22; Length 522;
 Query Match
                         Pred. No. 1.3e-252;
 Best Local Similarity
                    99.6%;
                                                    0; Gaps
 Matches 517; Conservative
                          1; Mismatches
                                           Indels
                                                             0;
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Qу
           4 MAVALRGLGGRFRWRTOAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAQLGR 63
Db
         61 KVAVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Qу
           64 KVSVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 123
Db
        121 DWRKMAEAVONHVKSLNWGHRVOLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
           124 DWRKMAEAVONHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 183
Db
        181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Qу
           184 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 243
Db
        241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
QУ
           244 TTIMMRSIPLRGFDOOMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDRTTGK 303
Db
        301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Qу
           Db
        304 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTOKILVDSREATSVPHIYAIGDVVEG 363
        361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Qу
           Db
        364 RPELTPTAIMAGRLLVORLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 423
        421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Qу
           424 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 483
Dh
Qу
        481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGC 519
           Dh
        484 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGC 522
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## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 5, 2003, 22:46:50; Search time 46 Seconds

(without alignments)

1797.751 Million cell updates/sec

Title: US-09-830-706B-2

Perfect score: 2744

Sequence: 1 MAVALRGLGGRFRWRTQAVA.....VKLRISKRSGLDPTVTGCXG 521

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 segs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseg 19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*

3: /SIDS1/gcqdata/geneseq/geneseqp-embl/AA1982.DAT:\*

4: /SIDS1/qcqdata/qeneseq/qeneseqp-emb1/AA1983.DAT:\*

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10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*

11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\*

12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*

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17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*

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19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*

20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:\*

21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*

23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

## SUMMARIES

		8				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	2742	99.9	521	21	AAB03787	Human SECIS encode
2	2742	99.9	521	21	AAB03751	Human thioredoxin
3	2736	99.7	521	23	ABP60944	Homo sapiens thior
4	2736	99.7	524	23	ABP60946	Homo sapiens thior
5	2733	99.6	524	23	ABP60941	Homo sapiens thior
6	2729	99.5	522	22	AAE05190	Human drug metabol
7	2716.5	99.0	521	23	ABP60949	Homo sapiens thior
8	2586	94.2	494	21	AAB03788	Human SECIS encode
9	2586	94.2	494	21	AAB03752	Human thioredoxin
10	2585	94.2	494	23	ABP60948	Homo sapiens thior
11	2355.5	85.8	524	23	ABP60954	Mus musculus thior
12	2354.5	85.8	520	23	ABP60956	Mus musculus thior
13	2352.5	85.7	528	23	ABP60955	Mus musculus thior
14	2318	84.5	526	23	ABP60963	Rattus norvegicus
15	2260.5	82.4	511	23	ABP60937	Bos taurus thiored
16	1461	53.2	613	23	ABP60951	Mus musculus thior
17	1460	53.2	499	23	ABP60957	Mus musculus thior
18	1442	52.6	499	23	ABP60879	Bos taurus thiored
19	1438	52.4	504	20	AAW83401	Human thioredoxin
20	1438	52.4	551	20	AAW83404	Human KM-102-deriv
21	1438	52.4	939	20	AAW83402	Human thioredoxin
22	1438	52.4	939	20	AAW83403	Human thioredoxin
23	1433	52.2	549	17	AAR92050	KM31-7 precursor.
24	1433	52.2	549	23	ABP60950	Homo sapiens thior
25	1426	52.0	497	23	ABP60942	Homo sapiens thior
26	1425	51.9	497	22	AAB90751	Human shear stress
27	1425	51.9	497	23	ABP60881	Homo sapiens thior
28	1425	51.9	497	24	AA020625	Thioredoxin reduct
29	1425	51.9	497	24	AAO20634	Thioredoxin reduct
30	1421.5	51.8	491	22	ABB58307	Drosophila melanog
31	1421.5	51.8	491	22	ABB67058	Drosophila melanog
32	1421	51.8	497	23	ABP60943	Homo sapiens thior
33	1421	51.8	498	22	AAB24181	Human brain thiore
34	1418	51.7	497	23	ABP60958	Rattus norvegicus
35	1418	51.7	499	23	ABP60964	Sus scrofa thiored
36	1414	51.5	497	23	ABP60701	Human thioredoxin
37	1410	51.4	579	23	ABP60945	Homo sapiens thior
38	1410	51.4	613	23	ABP60953	Mus musculus thior
39	1404	51.2	577	23	ABP60947	Homo sapiens thior
40	1403.5	51.1	498	23	ABP60960	Rattus norvegicus
41	1401	51.1	516	22	ABB65695	Drosophila melanog
42	1401	51.1	516	23	ABP60940	Drosophila melanog
43	1398.5	51.0	496	23	ABP60962	Rattus norvegicus
44	1306	47.6	667	23	ABP60939	Caenorhabditis ele
45	1300	47.4	525		ABP60938	Caenorhabditis ele
				-	- <del></del>	

```
RESULT 1
AAB03787
     AAB03787 standard; Protein; 521 AA.
ХX
AC
     AAB03787;
XX
DT
     13-OCT-2000 (first entry)
XX
     Human SECIS encoded protein sequence.
DE
XX
     Selenocysteine insertion sequence; SECIS; thioredoxin reductase;
KW
KW
     drug development; selenoprotein expression.
XX
OS
     Homo sapiens.
XX
                     Location/Qualifiers
FH
     Key
FT
     Modified-site
                     520
                     /label= Selenocysteine
FT
                     /note= "encoded by TGA"
FΤ
XX
DN
     WO200026358-A1.
XX
     11-MAY-2000.
PD
XX
ΡF
                    99WO-JP05984.
     28-OCT-1999;
XX
                    98JP-0310422.
PR
     30-OCT-1998;
     16-NOV-1998;
                    98JP-0325344.
PR
XX
PA
     (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PΙ
     Toji S, Yano M, Tamai K;
XX
DR
     WPI; 2000-376129/32.
DR
     N-PSDB; AAA59835.
XX
PT
     Novel selenocysteine insertion sequence which enforces reading of TGA
PT
     as selenocysteine in a translated region upstream of it, for expression
PT
     of selenoproteins -
XX
PS
     Disclosure; Page 38-42; 60pp; Japanese.
XX
CC
     The present invention relates to a Selenocysteine insertion sequence
CC
     which enforces the reading of a TGA codon as selenocysteine in a
     translated region upstream of it. The novel selenocysteine insertion
CC
CC
     sequence (SECIS) is of human thioredoxin reductase (TxR) origin. The
CC
     invention also includes an expression vector for selenoproteins
CC
     containing the new SECIS, a host cell transformed by the vector,
CC
     selenoproteins produced by the host cells, and a method for screening for
CC
     potential inhibitors of selenoprotein expression. The sequence is useful
     for the effective expression of selenoproteins and the development of
CC
CC
     drugs for treating disorders with which selenoproteins are associated.
     The present sequence represents a human amino acid sequence encoded by a
CC
CC
     SECIS containing nucleotide sequence.
XX
SO
     Sequence
                521 AA;
```

```
99.9%; Score 2742; DB 21; Length 521;
 Query Match
                    100.0%; Pred. No. 7.4e-254;
 Best Local Similarity
 Matches 521; Conservative
                        0; Mismatches
                                        0; Indels
                                                            0;
         1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
Qу
           Db
         1 MAVALRGLGGRFRWRTOAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
        61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Qу
           61 KVAVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHOAALLGGLIQDAPNYGWEVAQPVPH 120
Db
       121 DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
           121 DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Dh
       181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Qу
           181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Db
       241 TTIMMRSIPLRGFDOOMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
QУ
           241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
Db
       301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Qу
           301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Db
       361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Qу
           361 RPELTPTAIMAGRLLVORLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Db
       421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Qу
           421 VEVYHAHYKPLEFTVAGRDASOCYVKMVCLREPPOLVLGLHFLGPNAGEVTOGFALGIKC 480
Db
       481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Qу
           481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
RESULT 2
AAB03751
ID
   AAB03751 standard; Protein; 521 AA.
XX
AC
   AAB03751;
XX
DT
   04-OCT-2000
              (first entry)
XX
DE
   Human thioredoxin reductase (TxR) amino acid sequence.
XX
KW
   Thioredoxin reductase; TxR; human; inflammation; cancer; apoptosis;
KW
   X-linked inhibitor of apoptosis protein binding protein; XIAP;
   viral infection; chromosome 22g11.2.
KW
XX
os
   Homo sapiens.
```

XX

```
Misc-difference 521
FT
                   /note= "Selenocysteine"
FT
XX
ΡN
    WO200026382-A1.
XX
חק
    11-MAY-2000.
ХX
PF
    28-OCT-1999;
                 99WO-JP05983.
XX
    30-OCT-1998;
                98JP-0310422.
PR
ХX
    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PΑ
XX
PΙ
    Toji S, Yano M, Tamai K;
XX
DR
    WPI; 2000-365627/31.
    N-PSDB; AAA53429.
DR
XX
    Thioredoxin reductase II (an X-linked inhibitor for apoptosis protein
PΤ
    (XIAP) -binding protein), with thioredoxin reductase activity, useful
PT
    e.g. for treating apoptosis-related disorders, cancer and inflammation
РΤ
PT
XX
PS
    Claim 1; Page 53-56; 139pp; Japanese.
ХX
    This sequence represents a human thioredoxin reductase (TxR) protein
CC
    sequence. The invention relates to two TxR proteins, which have XIAP
CC
    (X-linked inhibitor of apoptosis protein)-binding protein activity. The
CC
    human TxR gene is located on chromosome 22q11.2. The invention includes
CC
    antibodies which bind to the proteins, a vector containing the TxR
CC
    encoding nucleotide sequences, and methods for producing transformants
CC
CC
    using the vector. Thioredoxin reductase has cytostatic and
    anti-inflammatory activity, and is used in the treatment of diseases
CC
    relating to apoptosis particularly due to cancer of viral infection. TxR
CC
    can also be used to treat inflammation and in the screening of
CC
    anti-cancer agents.
CC
XX
    Sequence
SO
              521 AA;
 Query Match
                        99.9%; Score 2742; DB 21; Length 521;
 Best Local Similarity 100.0%; Pred. No. 7.4e-254;
                                               0; Indels
 Matches 521; Conservative
                            0; Mismatches
                                                            0; Gaps
                                                                       0:
           1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
Qу
             1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
Db
          61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Qу
             61 KVAVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHOAALLGGLIQDAPNYGWEVAQPVPH 120
Db
         121 DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
             Db
         121 DWRKMAEAVONHVKSLNWGHRVOLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
         181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
QУ
```

Location/Oualifiers

FH

Key

```
Db
        181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
        241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
Qy
            241 TTIMMRSIPLRGFDOOMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGOLQVTWEDSTTGK 300
Db
        301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Qу
            301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTOKILVDSREATSVPHIYAIGDVVEG 360
Db
        361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Qу
            361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Db
        421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
QУ
            421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Db
        481 GASYAOVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Qу
            481 GASYAOVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Dh
RESULT 3
ABP60944
ID
    ABP60944 standard; Protein; 521 AA.
XX
AC
    ABP60944;
XX
DT
    06-SEP-2002 (first entry)
XX
DE
    Homo sapiens thioredoxin reductase SEQ ID NO:293.
XX
    Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
KW
    oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
KW
    vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;
KW
    food product; milk; wheat; oxidative stress; cataract; diabetes;
KW
    chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW
    bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW
    gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW
KW
    gastro oesophageal reflux disease.
XX
os
    Homo sapiens.
XX
PN
    WO200250289-A1.
XX
    27-JUN-2002.
חק
XX
PF
    19-DEC-2001; 2001WO-US50240.
XX
PR
    19-DEC-2000; 2000US-0742900.
    05-JUL-2001; 2001US-302885P.
PR
    04-DEC-2001; 2001US-0006038.
PR
XX
    (SEMB-) SEMBIOSYS GENETICS INC.
PΑ
    (SYGN ) SYNGENTA PARTICIPATIONS AG.
PΑ
```

```
XX
PΙ
    Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
PΙ
    Del Val G, Zaplachinski S, Moloney M;
XX
DR
    WPI; 2002-508806/54.
XX
PТ
    Producing oil body associated with recombinant multimeric protein
    complex e.g. redox proteins and immunoglobulins comprises producing
PΤ
    recombinant polypeptides capable of forming the complex in cells
PΤ
PT
    comprising oil bodies -
XX
PS
    Claim 82; Page 337-338; 362pp; English.
XX
    The present invention describes a method (M1) for producing an oil body
CC
    associated with a recombinant multimeric protein complex (MPC). M1
CC
    comprises producing in a cell comprising oil bodies a first and second
CC
CC
    recombinant polypeptide (P1, P2), where P1 is capable of associating
    with P2 to form the MPC and associating the complex with an occlusion
CC
CC
    body (OB) through an OB-targeting-protein capable of associating with OB
CC
    and P1. M1 is useful for producing an oil body associated with a
    recombinant MPC. The oil bodies are further formulated for use in the
CC
CC
    preparation of a food product such as milk or wheat based food product,
    personal care product which reduces the oxidative stress on the surface
CC
CC
    area of the human body or used to lighten the skin, or a pharmaceutical
CC
    composition used to treat chronic obstructive pulmonary disease (COPD),
CC
    cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC
    malignancies, reperfusion injury, wound healing, sepsis, gastro
CC
    intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC
    (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677
CC
    to ABP60964 represent sequence given in the exemplification of the
CC
    present invention.
XX
SO
    Sequence
              521 AA;
 Ouery Match
                       99.7%; Score 2736; DB 23; Length 521;
 Best Local Similarity
                       99.8%; Pred. No. 2.8e-253;
 Matches 520; Conservative
                            0; Mismatches
                                                          0;
                                              1; Indels
                                                                     0;
                                                              Gaps
           1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAQLGR 60
QУ
            1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
Db
Qу
          61 KVAVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHOAALLGGLIODAPNYGWEVAOPVPH 120
            Db
          61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
         121 DWRKMAEAVONHVKSLNWGHRVQLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
            121 DWRKMAEAVONHVKSLNWGHRVQLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Db
         181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Qу
            181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Db
Qу
         241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
            241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
Db
```

```
301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Qу
            301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Db
         361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Qу
            361 RPELTPIAIMAGRLLVORLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Db
         421 VEVYHAHYKPLEFTVAGRDASOCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Qу
            421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Db
         481 GASYAOVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
QУ
            481 GASYAOVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Db
RESULT 4
ABP60946
    ABP60946 standard; Protein; 524 AA.
XX
AC
    ABP60946;
XX
DT
    06-SEP-2002 (first entry)
XX
    Homo sapiens thioredoxin reductase SEQ ID NO:295.
DE
XX
KW
    Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
    oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
KW
    vasotropic; vulnerary; antibacterial; immunosuppressive; antiulcer;
KW
    food product; milk; wheat; oxidative stress; cataract; diabetes;
KW
    chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW
    bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW
    gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW
KW
    gastro oesophageal reflux disease.
XX
OS
    Homo sapiens.
XX
PN
    WO200250289-A1.
XX
    27-JUN-2002.
PD
XX
    19-DEC-2001; 2001WO-US50240.
PF
XX
PR
    19-DEC-2000; 2000US-0742900.
    05-JUL-2001; 2001US-302885P.
PR
PR
    04-DEC-2001; 2001US-0006038.
XX
    (SEMB-) SEMBIOSYS GENETICS INC.
PA
    (SYGN ) SYNGENTA PARTICIPATIONS AG.
PA
XX
PΤ
    Van Rooijen G, Deckers H, Heifetz PB,
                                         Briggs SP, Dalmia BK;
PΙ
    Del Val G, Zaplachinski S, Moloney M;
XX
DR
    WPI; 2002-508806/54.
XX
```

Producing oil body associated with recombinant multimeric protein DТ РТ complex e.q. redox proteins and immunoglobulins comprises producing PT recombinant polypeptides capable of forming the complex in cells comprising oil bodies -PT XX PS Claim 82; Page 340-341; 362pp; English. XX The present invention describes a method (M1) for producing an oil body CC associated with a recombinant multimeric protein complex (MPC). M1 CC CC comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating CC with P2 to form the MPC and associating the complex with an occlusion CC body (OB) through an OB-targeting-protein capable of associating with OB CC and P1. M1 is useful for producing an oil body associated with a CC recombinant MPC. The oil bodies are further formulated for use in the CC preparation of a food product such as milk or wheat based food product, CC personal care product which reduces the oxidative stress on the surface CC area of the human body or used to lighten the skin, or a pharmaceutical CC composition used to treat chronic obstructive pulmonary disease (COPD), CC cataracts, diabetes, envenomation, bronchiopulmonary disease, psoriasis, CC CC malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD CC CC (qastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to ABP60964 represent sequence given in the exemplification of the CC CC present invention. XX SQ Sequence 524 AA; 99.7%; Score 2736; DB 23; Length 524; Query Match 99.8%; Pred. No. 2.8e-253; Best Local Similarity 0; Mismatches Matches 520; Conservative 1; Indels 0; 1 MAVALRGLGGRFRWRTOAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAQLGR 60 Qу 4 MAVALRGLGGRFRWRTOAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAOLGR 63 Db Qу 61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120 64 KVAVVDYVEPSPOGTRWGLGGTCVNVGCIPKKLMHOAALLGGLIODAPNYGWEVAOPVPH 123 Dh QУ 121 DWRKMAEAVONHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180 124 DWRKMAEAVONHVKSLNWGHRVOLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 183 Dh 181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240 Qу 184 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 243 Db Qy 241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300 244 TTIMMRSIPLRGFDOOMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 303 Db Qу 301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360

> 361 RPELTPTAIMAGRLLVORLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGOEH 420

Db

Ov

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 5, 2003, 22:54:46; Search time 46 Seconds

(without alignments)

1797.751 Million cell updates/sec

Title: US-09-830-706B-2

Perfect score: 521

Sequence: 1 MAVALRGLGGRFRWRTQAVA.....VKLRISKRSGLDPTVTGCXG 521

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 1107863 segs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq 19Jun03:\*

1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\* 2: /SIDS1/gcqdata/geneseq/geneseqp-embl/AA1981.DAT:\* 3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\* 4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\* 5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\* 6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\* 7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\* 8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\* 9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\* 10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\* 11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:\* 12: /SIDS1/qcqdata/qeneseq/qeneseqp-embl/AA1991.DAT:\* 13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\* 14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\* 15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\* 16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\* 17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\* 18: 19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\* 20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\* 21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:\* 22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\* 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\* 24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		₹				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	520	99.8	521	21	AAB03787	Human SECIS encode
2	520	99.8	521	21	AAB03751	Human thioredoxin
3	489	93.9	494	21	AAB03788	Human SECIS encode
4	489	93.9	494	21	AAB03752	Human thioredoxin
5	488	93.7	494	23	ABP60948	Homo sapiens thior
6	419	80.4	521	23	ABP60944	Homo sapiens thior
7	419	80.4	524	23	ABP60946	Homo sapiens thior
8	356	68.3	524	23	ABP60941	Homo sapiens thior
9	355	68.1	521	23	ABP60949	Homo sapiens thior
10	355	68.1	522	22	AAE05190	Human drug metabol
11	214	41.1	234	21	AAB58986	Breast and ovarian
12	46	8.8	520	23	ABP60956	Mus musculu

```
RESULT 1
AAB03787
     AAB03787 standard; Protein; 521 AA.
ХX
AC
     AAB03787;
XX
DT
     13-OCT-2000 (first entry)
XX
     Human SECIS encoded protein sequence.
DΕ
XX
     Selenocysteine insertion sequence; SECIS; thioredoxin reductase;
KW
     drug development; selenoprotein expression.
KW
XX
os
     Homo sapiens.
XX
                     Location/Qualifiers
FH
     Kev
     Modified-site
                     520
FT
FT
                     /label= Selenocysteine
FT
                     /note= "encoded by TGA"
XX
     WO200026358-A1.
PN
ХX
PD
     11-MAY-2000.
XX
PF
     28-OCT-1999;
                    99WO-JP05984.
XX
     30-OCT-1998;
PR
                    98JP-0310422.
     16-NOV-1998;
                    98JP-0325344.
PR
XX
     (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
PΑ
XX
PΙ
     Toji S, Yano M, Tamai K;
XX
DR
     WPI; 2000-376129/32.
     N-PSDB; AAA59835.
DR
XX
     Novel selenocysteine insertion sequence which enforces reading of TGA
PT
     as selenocysteine in a translated region upstream of it, for expression
PT
     of selenoproteins -
PT
XX
PS
     Disclosure; Page 38-42; 60pp; Japanese.
XX
CC
     The present invention relates to a Selenocysteine insertion sequence
     which enforces the reading of a TGA codon as selenocysteine in a
CC
CC
     translated region upstream of it. The novel selenocysteine insertion
     sequence (SECIS) is of human thioredoxin reductase (TxR) origin. The
CC
CC
     invention also includes an expression vector for selenoproteins
CC
     containing the new SECIS, a host cell transformed by the vector,
CC
     selenoproteins produced by the host cells, and a method for screening for
     potential inhibitors of selenoprotein expression. The sequence is useful
CC
     for the effective expression of selenoproteins and the development of
CC
     drugs for treating disorders with which selenoproteins are associated.
CC
CC
     The present sequence represents a human amino acid sequence encoded by a
CC
     SECIS containing nucleotide sequence.
XX
SO
     Sequence
                521 AA;
```

```
99.8%; Score 520; DB 21; Length 521;
 Query Match
 Best Local Similarity
                    100.0%; Pred. No. 0;
                         0; Mismatches
 Matches 521; Conservative
                                        0; Indels
                                                   0; Gaps
                                                            0;
         1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
Qy
           1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGQRDYDLLVVGGGSGGLACAKEAAQLGR 60
Db
        61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Qу
           61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Db
       121 DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
           121 DWRKMAEAVONHVKSLNWGHRVOLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Db
       181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Qу
           181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Db
       241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
QУ
           241 TTIMMRSIPLRGFDOOMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
Db
Qу
       301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTOKILVDSREATSVPHIYAIGDVVEG 360
           301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
Db
       361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Qу
           361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Db
       421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Qу
           421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Db
       481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
Qу
           Db
       481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
RESULT 2
AAB03751
ID
    AAB03751 standard; Protein; 521 AA.
XX
AC
    AAB03751;
XX
DT
    04-OCT-2000
              (first entry)
XX
DE
    Human thioredoxin reductase (TxR) amino acid sequence.
XX
KW
    Thioredoxin reductase; TxR; human; inflammation; cancer; apoptosis;
    X-linked inhibitor of apoptosis protein binding protein; XIAP;
KW
KW
    viral infection; chromosome 22g11.2.
XX
os
    Homo sapiens.
```

XX

```
FT
    Misc-difference 521
FT
                   /note= "Selenocysteine"
XX
PN
    W0200026382-A1.
XX
PD
    11-MAY-2000.
XX
PF
    28-OCT-1999;
                  99WO-JP05983.
XX
PŔ
    30-OCT-1998;
                  98JP-0310422.
XX
PΑ
     (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
ΡI
    Toji S, Yano M, Tamai K;
XX
DR
    WPI; 2000-365627/31.
    N-PSDB; AAA53429.
DR
XX
PΤ
    Thioredoxin reductase II (an X-linked inhibitor for apoptosis protein
PT
    (XIAP) -binding protein), with thioredoxin reductase activity, useful
PΤ
    e.g. for treating apoptosis-related disorders, cancer and inflammation
PT
XX
PS
    Claim 1; Page 53-56; 139pp; Japanese.
XX
CC
    This sequence represents a human thioredoxin reductase (TxR) protein
CC
    sequence. The invention relates to two TxR proteins, which have XIAP
CC
    (X-linked inhibitor of apoptosis protein) -binding protein activity. The
CC
    human TxR gene is located on chromosome 22q11.2. The invention includes
CC
    antibodies which bind to the proteins, a vector containing the TxR
CC
    encoding nucleotide sequences, and methods for producing transformants
CC
    using the vector. Thioredoxin reductase has cytostatic and
CC
    anti-inflammatory activity, and is used in the treatment of diseases
CC
    relating to apoptosis particularly due to cancer of viral infection. TxR
CC
    can also be used to treat inflammation and in the screening of
CC
    anti-cancer agents.
XX
so
    Sequence
              521 AA;
 Query Match
                        99.8%; Score 520; DB 21; Length 521;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 521; Conservative 0; Mismatches
                                               0; Indels
                                                            0; Gaps
                                                                       0:
Qу
           1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAOLGR 60
             Db
           1 MAVALRGLGGRFRWRTQAVAGGVRGAARGAAAGORDYDLLVVGGGSGGLACAKEAAOLGR 60
          61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHQAALLGGLIQDAPNYGWEVAQPVPH 120
Qу
             Db
          61 KVAVVDYVEPSPQGTRWGLGGTCVNVGCIPKKLMHOAALLGGLIODAPNYGWEVAOPVPH 120
Qу
         121 DWRKMAEAVQNHVKSLNWGHRVQLQDRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
             Db
         121 DWRKMAEAVONHVKSLNWGHRVOLODRKVKYFNIKASFVDEHTVCGVAKGGKEILLSADH 180
Qу
         181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
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Location/Qualifiers

FΗ

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181 IIIATGGRPRYPTHIEGALEYGITSDDIFWLKESPGKTLVVGASYVALECAGFLTGIGLD 240
Db
        241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
Qу
            Db
        241 TTIMMRSIPLRGFDQQMSSMVIEHMASHGTRFLRGCAPSRVRRLPDGQLQVTWEDSTTGK 300
        301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTQKILVDSREATSVPHIYAIGDVVEG 360
QУ
            301 EDTGTFDTVLWAIGRVPDTRSLNLEKAGVDTSPDTOKILVDSREATSVPHIYAIGDVVEG 360
Db
Qу
        361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
            Db
        361 RPELTPTAIMAGRLLVQRLFGGSSDLMDYDNVPTTVFTPLEYGCVGLSEEEAVARHGQEH 420
Qу
        421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
            Db
        421 VEVYHAHYKPLEFTVAGRDASQCYVKMVCLREPPQLVLGLHFLGPNAGEVTQGFALGIKC 480
Qу
        481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
           Db
        481 GASYAQVMRTVGIHPTCSEEVVKLRISKRSGLDPTVTGCXG 521
RESULT 3
AAB03788
ID
    AAB03788 standard; Protein; 494 AA.
XX
AC
    AAB03788;
XX
DT
    13-OCT-2000 (first entry)
XX
DE
    Human SECIS encoded protein sequence.
XX
KW
    Selenocysteine insertion sequence; SECIS; thioredoxin reductase;
KW
    drug development; selenoprotein expression.
ХX
OS
    Homo sapiens.
XX
FH
    Key
                 Location/Qualifiers
FT
    Modified-site
FT
                 /label= Selenocysteine
FT
                 /note= "encoded by TGA"
XX
PN
    WO200026358-A1.
XX
PD
    11-MAY-2000.
XX
PF
    28-OCT-1999;
                99WO-JP05984.
XX
PR
    30-OCT-1998;
                98JP-0310422.
    16-NOV-1998;
PR
                98JP-0325344.
ΧX
PΑ
    (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
ΡI
    Toji S, Yano M, Tamai K;
XX
```

```
WPI; 2000-376129/32.
DR
    N-PSDB: AAA59836.
DR
XX
    Novel selenocysteine insertion sequence which enforces reading of TGA
PТ
    as selenocysteine in a translated region upstream of it, for expression
PT
PT
    of selenoproteins -
XX
PS
    Disclosure; Page 48-52; 60pp; Japanese.
XX
    The present invention relates to a Selenocysteine insertion sequence
CC
    which enforces the reading of a TGA codon as selenocysteine in a
CC
    translated region upstream of it. The novel selenocysteine insertion
CC
    sequence (SECIS) is of human thioredoxin reductase (TxR) origin. The
CC
    invention also includes an expression vector for selenoproteins
CC
    containing the new SECIS, a host cell transformed by the vector,
CC
    selenoproteins produced by the host cells, and a method for screening for
CC
    potential inhibitors of selenoprotein expression. The sequence is useful
CC
    for the effective expression of selenoproteins and the development of
CC
    drugs for treating disorders with which selenoproteins are associated.
CC
    The present sequence represents a human amino acid sequence encoded by a
CC
    SECIS containing nucleotide sequence.
CC
ХX
    Sequence
SQ
             494 AA;
 Query Match
                      93.9%; Score 489; DB 21; Length 494;
 Best Local Similarity
                      100.0%; Pred. No. 0;
 Matches 490; Conservative
                                                       0; Gaps
                                                                  0:
                          0; Mismatches
                                           0; Indels
         32 AGORDYDLLVVGGGSGGLACAKEAAOLGRKVAVVDYVEPSPQGTRWGLGGTCVNVGCIPK 91
Qу
            5 AGQRDYDLLVVGGGSGGLACAKEAAQLGRKVAVVDYVEPSPQGTRWGLGGTCVNVGCIPK 64
Db
         92 KLMHQAALLGGLIQDAPNYGWEVAQPVPHDWRKMAEAVQNHVKSLNWGHRVQLQDRKVKY 151
Qу
            65 KLMHOAALLGGLIODAPNYGWEVAOPVPHDWRKMAEAVONHVKSLNWGHRVOLQDRKVKY 124
Db
        152 FNIKASFVDEHTVCGVAKGGKEILLSADHIIIATGGRPRYPTHIEGALEYGITSDDIFWL 211
Qу
            125 FNIKASFVDEHTVCGVAKGGKEILLSADHIIIATGGRPRYPTHIEGALEYGITSDDIFWL 184
Db
        212 KESPGKTLVVGASYVALECAGFLTGIGLDTTIMMRSIPLRGFDQQMSSMVIEHMASHGTR 271
Qу
            Db
        185 KESPGKTLVVGASYVALECAGFLTGIGLDTTIMMRSIPLRGFDQOMSSMVIEHMASHGTR 244
        272 FLRGCAPSRVRRLPDGQLQVTWEDSTTGKEDTGTFDTVLWAIGRVPDTRSLNLEKAGVDT 331
Qу
            245 FLRGCAPSRVRRLPDGOLOVTWEDSTTGKEDTGTFDTVLWAIGRVPDTRSLNLEKAGVDT 304
Db
        332 SPDTQKILVDSREATSVPHIYAIGDVVEGRPELTPTAIMAGRLLVQRLFGGSSDLMDYDN 391
Qу
            305 SPDTQKILVDSREATSVPHIYAIGDVVEGRPELTPTAIMAGRLLVORLFGGSSDLMDYDN 364
Db
Qу
        392 VPTTVFTPLEYGCVGLSEEEAVARHGOEHVEVYHAHYKPLEFTVAGRDASQCYVKMVCLR 451
            365 VPTTVFTPLEYGCVGLSEEEAVARHGQEHVEVYHAHYKPLEFTVAGRDASQCYVKMVCLR 424
Db
```

452 EPPQLVLGLHFLGPNAGEVTOGFALGIKCGASYAOVMRTVGIHPTCSEEVVKLRISKRSG 511

Qу

Db

512 LDPTVTGCXG 521 Qу

||||||||| 485 LDPTVTGCXG 494

Db